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Genetic diversity and architecture of gene expression in response to water deficit in tomato

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Tomato is both a model species thanks to the large genetic and genomic resources available and an important crop. Tomato fruit quality is characterized by a large number of components influenced by the genotypes and the environment, notably water status. In order to unravel the genetic control of these components, quantitative trait loci for transcript amount (eQTL), metabolic and phenotypic traits (phQTL) have been mapped under control and water deficit conditions. We used a RIL population derived from an intraspecific cross between a cherry tomato line and a large fruited line. The genomes of both parents were sequenced and differ by more than 2 million SNPs. RNAseq of parental lines revealed a number of functions affected by water stress, but also some major differences according to the parents. On the RIL population we harvested fruit and leaf samples and performed eQTL mapping for 270 differentially expressed genes using the fluidigm technology. Several eQTL were mapped, some with strong effects, a majority of which acting as cis eQTL, and clusters of eQTL and pQTL were demonstrated. Analysis of the transcriptome of the F1 hybrid allowed the quantification of allele specific expression and identification of almost 2000 cis-regulated genes and 1,450 *trans* regulated genes. Contrary to *trans* regulatory divergences, *cis* regulatory divergences were strongly conserved between organs and between watering regimes. Results will be discussed in regard to the gene functions and co-localisations with metabolite or phenotype pQTLs.